

## REVIEW

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## A review on machine learning algorithms for the ionic liquid chemical space†

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There are thousands of papers published every year investigating the properties and possible applications of ionic liquids. Industrial use of these exceptional fluids requires adequate understanding of their physical properties, in order to create the ionic liquid that will optimally suit the application. Computational property prediction arose from the urgent need to minimise the time and cost that would be required to experimentally test different combinations of ions. This review discusses the use of machine learning algorithms as property prediction tools for ionic liquids (either as standalone methods or in conjunction with molecular dynamics simulations), presents common problems of training datasets and proposes ways that could lead to more accurate and efficient models.

## Introduction

Over the past decades, ionic liquids (ILs) have been a topic of intensive research worldwide. A simple search of the term “ionic liquids” at the Web of Science shows thousands of new papers

being published each year, with almost 9000 papers being published in 2020, even excluding the newer trend for Deep Eutectic Solvents. This phenomenon is very much expected, considering that there is a worldwide need to increase the efficiency of industrial processes, while reducing their ecological footprint.<sup>1</sup> ILs are highly promising materials for this goal, as they can be fine-tuned to fit the needs of a specific application, while their thermal and chemical stabilities and negligible vapour pressures make them easily recyclable. According to numerous studies, ILs can be ideal candidates for a plethora of different applications such as reaction solvents, catalysts,

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lubricants, electrolytes, extraction media, drug delivery systems *etc.*<sup>2–5</sup>

The synthetic flexibility associated with ILs has led to them being described as ‘designer solvents’.<sup>6</sup> However, throughout their history there has been insufficient understanding of how the properties of ionic liquids arise from the molecular structures of their constituent ions. Until recently, the usual way of studying and understanding the properties of ILs was essentially by trial and error. Researchers, based on their empirical knowledge and intuitive understanding of ILs and their properties, conceptualised a combination of anions and cations that could have the desired properties and then made homologous series of ILs – hoping that even if the initial attempt was fruitless they would get sufficient feedback to achieve the required properties with a second attempt. However, this method is time-consuming and expensive. Therefore, the need for a prediction, or at least an initial estimation, of the emergent properties of any IL based solely on the structures of its ions becomes evident. Many experts on ILs have indicated that the significant lack of physical data impedes their industrial commercialisation.<sup>7</sup>

Structure–Property Relationship (SPR) has been studied for many years, with major applications being polymer and pharmaceutical research.<sup>8–10</sup> SPR has been studied from early in IL research, since the natures of the anions and cations, and the interactions between these are usually directly translated to the IL's physical properties.<sup>11</sup> Therefore, there is a quite extensive qualitative understanding of the basic properties of very popular IL families, which makes it easy for the researchers to find an IL with ‘low melting point’, ‘a wide electrochemical window’ or ‘increased hydrophobicity’. However, in practise the knowledge of general physicochemical characteristics of an IL family is not sufficient when the researcher wants to design tailor-made ILs for specific applications. In this case an accurate prediction of the properties is required that goes beyond the generalities of ‘low viscosity’ or ‘high conductivity’. There is the

need for quantitative structure–property relationship (QSPR) studies and the creation of mathematical models that can predict accurate numerical results based solely on structural data of the IL.<sup>12,13</sup>

QSPR for ILs is a difficult and computationally challenging research area, something that can be understood from the fact that there are fewer available predictive models than for other commonly used chemicals (such as pharmaceuticals or molecular solvents). The difficulty lies in the complexity of inter- and intramolecular interactions and that these interactions are not completely understood for all types of ILs. Every experimentalist researcher of ILs has experienced making ILs that don't behave as they expected. This can result in modifying the existing theories in order to rationalise and include those outliers – a process which can prove extremely time consuming – or often to that particular IL being excluded from future studies.

In 1952, computer scientist Arthur Samuel created his famous checkers playing program, introducing a new era for Computer Science, the field of artificial intelligence.<sup>14</sup> Samuel's checkers player was the first program that could learn while it was running and become a better player after each game. The idea that a program could evolve on its own, without the need of manual modifications on the code, was a technological milestone that would have a major impact in the evolution of Computer Science. Fast forward to the 21<sup>st</sup> Century, and the evolution of the calculation power of modern computing systems has given machine learning methods (ML) the capacity to perform complicated calculations with extreme time and resources efficiency which are being used by major technological companies.<sup>15</sup> There are many detailed manuscripts on the history and evolution of ML, some indicative works are cited here.<sup>16,17</sup>

ML methods are currently being implemented in research in a wide range of scientific fields, including chemical discovery and molecular design.<sup>18</sup> The secret behind their popularity is that in a space of unlimited molecules and synthetic pathways,



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*macroscopic behaviours. He is particularly interested in how ionic liquids influence solute behaviours and to use this understanding to provide more effective chemical processes. Much of his current work focusses on using ionic liquids to make biomass derived chemicals and materials.*



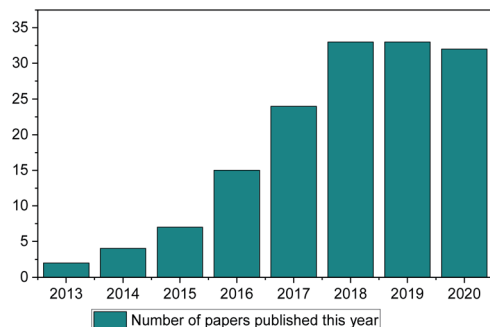


Fig. 1 Web of science search of "Ionic Liquids" and "Machine Learning" (search January 2021).

ML can use complex statistical systems to provide the researcher with a view of greater possibilities to guide their research.<sup>19</sup> In contrast to other fields (such as drug discovery, toxicology research, synthetic pathways *etc.*) ML has only been used in IL discovery over the past decade, with only a small number of published papers (Fig. 1). This is the main point of discussion of this review paper. Why in an otherwise very much computer-aided research field (there are thousands of available papers on molecular dynamics, Monte-Carlo, *ab initio* *etc.* calculations) is there so limited literature on ML methods for properties prediction?

## Presentation of the ML methods used in IL research

In order for this work to be helpful, we have to present some short definitions and descriptions of significant terms that will be very frequently used below. Artificial Intelligence (AI) is a term which, nowadays, it is being widely used – without being followed by a strict definition. According to the very popular textbook by Russel and Norvig, AI refers to the "creation of human-like behaviour which can plan, learn, perceive or process a natural language".<sup>20</sup> The term intelligence as applied to computers is different to intelligence as it is used in the everyday world. An intelligent machine is not necessarily one that can perform very difficult calculations, but rather a machine that gets feedback from the results it produces and re-uses these in order to continuously improve its methods.<sup>21</sup>

Machine learning refers to the creation of algorithms, a sequence of guidelines that help the computer to solve a specific task, sorting and correlating enormous amounts of data. ML offers the computer an automated step-by-step learning capability, enabling it to perform complicated tasks that the user could not program by hand.<sup>22</sup> These algorithms use statistics in order to correlate large data sets. Input data are fed to the ML learning algorithm, which by using a so-called task-specific feature extractor creates a series of constructed artificial features. The artificial features, which do not necessarily correspond to physical properties of the chemical system being studied, become the input for the regression algorithm (or classifier), which tries to correlate these with the studied

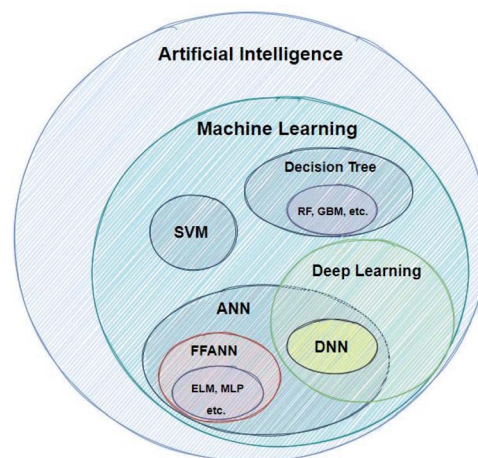


Fig. 2 Categorisation of AI computational methods discussed in this work.

property (modelling). There are a great number of different techniques developed for modelling, such as Support Vector Machines (SVMs), Artificial Neural Networks (ANNs) *etc.*<sup>23</sup> Fig. 2 shows the AI methods that are discussed in this work.

A crucial point in ML methods is data representation. For many years the bottleneck of ML research was the construction of feature extractors that could transform raw data to a format suitable for the algorithm. This led to the discovery and flourishing of Deep Learning (DL) techniques, which are methods with multiple levels of representation of data.<sup>24</sup> Raw data go through multiple non-linear nodes, which transform the initial representation to another – usually more abstract – form, which then makes it much easier for the algorithm to fit very complex equations (Fig. 3).

In order for the reader to better understand the advantages and limitations of the methods discussed further below, we believe it is crucial to have an adequate understanding of the concepts of over- and underfitting. Most regression models are not supposed to go through all the given data points, instead they are creating the curve with the minimum possible residual distance from the measured points.<sup>26</sup> Overfitting is the modelling error that occurs when the function is fit too closely to a limited set of data and it is a common problem when an algorithm creates an excessively complex model (with too many parameters). As a result, the model picks noise or random fluctuations and considers them as parts of the function. On the other hand, underfitting refers to the case when the created function can't capture the complexity of the data space and wrongly over-simplifies it. An underfit model can neither model the training data nor create/predict new data points.<sup>27</sup>

The obvious question arising from this discussion is "how many parameters are enough?". This is not an easily-answered question, as this really depends on the complexity of the contributions to the phenomenon being investigated. Enrico Fermi in 1953 was asked whether he was impressed with the agreement between his measured data and computationally calculated values performed by other groups. In his reply he





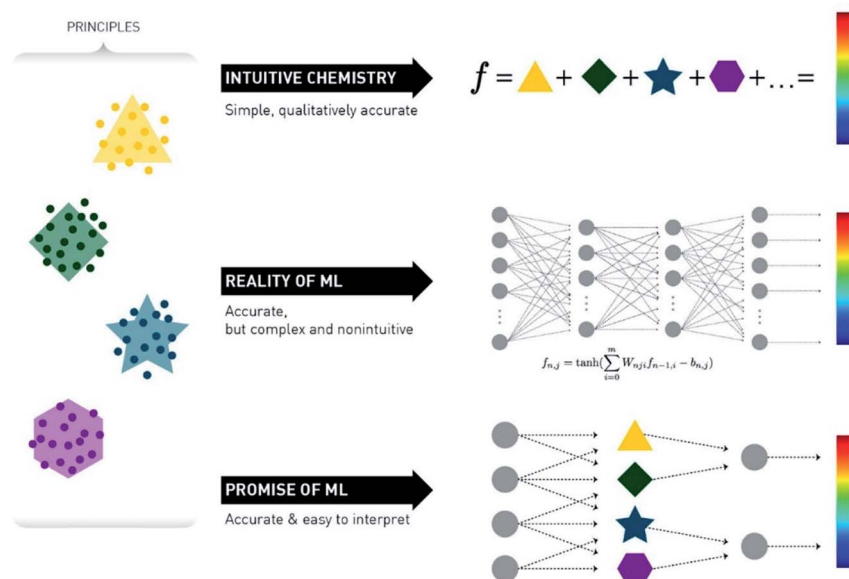


Fig. 3 Schematic representation of the promise *versus* reality of the use of ML for chemical reaction prediction. Reprinted with permission from Kammeraad *et al.*<sup>25</sup> Copyright 2020 American Chemical Society.

quoted Johnny von Neumann saying ‘with four parameters I can fit an elephant and with five I can make him wiggle his trunk’.<sup>28</sup> This anecdote has given rise to a debate among theoreticians, trying to prove whether it is actually possible, but has indicated a very significant point of computational research, that the complexity or arbitrariness of parameters can play a crucial role in statistical fitting of measured data.<sup>29,30</sup>

Artificial Neural Networks (ANNs), which constitute the basis for most DL algorithms, consist of large successive layers of processing units which lead to different levels of representations and therefore different levels of learned abstraction (see Fig. 4 and 5).<sup>31</sup> Conventional ANNs get as input the artificial features from the raw data and layer after layer, try to correlate these with the studied property – until they reach the final layer which is property prediction.

Advances in DL algorithms have led to further evolution of ANNs: Deep Neural Networks (DNNs). These methods learn

specific patterns extracted directly from the raw data (automatic feature extraction), rather than the extracted features used by conventional ML methods. Furthermore, they are more computationally efficient in finding non-linear correlations. Following the principles of DL, non-linear transformations can be applied from one layer to the next and so on, thus creating an algorithm that can more easily learn more abstract features.<sup>32</sup> Although they are not identical, the terms ANN and DNN are often interchanged in the literature, making it difficult for a reader with limited knowledge of the subject to directly understand the used method.

However, DNNs have their flaws, which have to do mainly with the existence of many hyperparameters, parameters whose values define the network’s structure and guide the training process, which require a lot of computational time and effort to fine-tune. Moreover, because of the numerous layers and their incredible correlation capacity, they are very vulnerable to overfitting the data – as they tend to recognise and model rare correlations that appear in the dataset, but might not actually have physical significance.<sup>34</sup>

Although ANNs are arguably the most widely used AI technique in chemical research (and many other fields), they do have their flaws and some researchers look for alternatives. The most significant disadvantages relevant to chemical research are the strong dependence between input and output, long training times with many epochs (number of passes of the training set completed by the algorithm), the need for very large and diverse datasets and their susceptibility to overfitting.<sup>35,36</sup> Trying to overcome these problems, many researchers turn to Support Vector Machines (SVM), which at least in the case of IL property prediction, is the second most popular method of choice.

SVMs work on the simple rule of depicting the training data as vectors in space and trying to categorise these with the widest

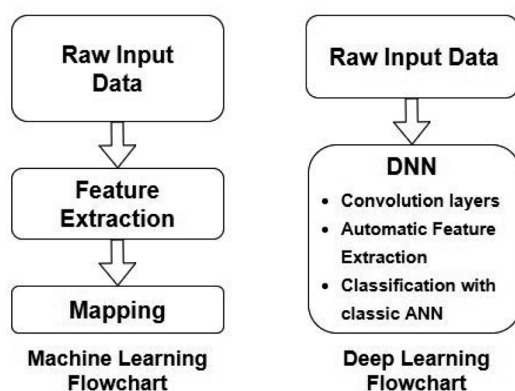
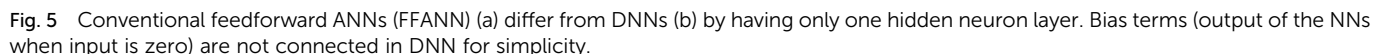


Fig. 4 Comparison between conventional ML and DL workflows. Redrawn from Visvikis *et al.*<sup>33</sup>





DTs have a fundamental disadvantage in that a simple tree structure suffers from a large bias, while a complex tree has a large variance. In order to overcome these problems, researchers use various ensemble methods, which try to group together many simple trees (weak learners) in order to create a strong learner.<sup>48</sup> There are two basic categories of ensemble methods, bagging and boosting. Bagging aims to reduce the variance of a DT by splitting the training data to subsets, training different trees and use an average of those models – which has proven as more efficient than a single DT. Random Forest (RF) is an extension of bagging, which as an addition uses a subset of the existing predictive features, instead of using all of them to grow the trees. RF offers the advantage of handling better high dimensional data.<sup>49</sup> Boosting is the ensemble method which creates a sequence of many simple trees (weak learners) in order to achieve one strong learner. Each tree is focused on reducing the fitting error received from

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graph TD; Root((Root Node)) --> D1[Decision Node]; Root --> D2[Decision Node]; D1 --> L1((Leaf Node)); D1 --> L2((Leaf Node)); D2 --> D3[Decision Node]; D2 --> L3((Leaf Node)); D3 --> L4((Leaf Node)); D3 --> L5((Leaf Node));
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Feature with the highest predictive power is used to split the tree at the **root node**.

Each split results in a more homogeneous dataset.

Sub-Tree

Decision Node

Leaf Node

Decision Node

A feature of the dataset is tested against a certain value and based on the results the further expansion of the tree is decided.

Decision Node

Leaf Node

The tree is not expanded further, because it has fulfilled some end condition (The dataset is homogeneous enough based on that feature).

Leaf Node

Leaf Node

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the previous tree. Gradient boosting is an extension of this method, which uses of a loss function that detects residuals. New learners fit to the residuals from previous steps, trying to recover the loss (difference between actual and predicted value) so that the model improves faster.<sup>50</sup> A basic advantage of the Gradient Boosting method is that it supports the use of different kinds of loss functions (higher versatility) and also it provides accurate results even if there are interactions between the studied parameters.<sup>48</sup>

## ILs as input data

When QSPR models are being set up, a major decision point is how the researchers will translate chemistry to maths. QSPR correlations can use input data either directly from experimental measurements or create descriptors based upon the molecular structure. The vast majority of properties prediction methods (both classical computational and ML methods) for complex molecules are based on group-contribution theory (GC).<sup>51–54</sup> GC models break down molecules into characteristic sub-structures (descriptors), which then can be correlated with specific effects on the compound's properties. The simplest, and most used, GC models study first-order correlations between the model and the studied property, in which the property arises as a simple sum of the contributing factors. Over recent years, the increase in the available computational power has made more complicated second and third order models more popular (eqn (1)).<sup>55</sup>

$$f(X) = \sum N_i A_i + \sum M_j B_j + \sum W_k C_k \quad (1)$$

$f(X)$  is the value of a studied property  $X$  at given conditions (*e.g.* viscosity at given temperature and pressure),  $A_i$ ,  $B_j$  and  $C_k$  are first, second and third order contribution factors – corresponding to the number of performed regressions,  $N$ ,  $M$  and  $W$  show how many of each factor appears in a molecule.

The number of descriptors and the complexity of chemical structures are significant parameters that affect the results of the model, but they are decided on a trial-and-error basis with each researcher following a different route. Especially for IL systems, the occurring interactions are numerous and complex. Therefore, there are limitations on how accurately somebody can depict an IL with such descriptors.<sup>56</sup> ML models are usually data-hungry and if not properly adjusted they tend to create hundreds of parameters and overfit the results – something that should be avoided by all means. The general rule is that the model should remain as simple as possible, to give meaningful predictions and as general as possible, in order to be able to encompass a large range of molecules. Moreover, there are studies that show that, in some cases, increasing the order of the correlation factor makes the models more complicated but does not actually improve their accuracy.<sup>57</sup>

Another method of transforming chemical structures to descriptors was introduced by Valderrama *et al.*<sup>58,59</sup> Their mass connectivity index (MCI) offers the capability, by using simple calculations, to connect the mass of the functional groups in a molecule with the type of connection (branching, double

bonds *etc.*). However, the simplicity of the method comes with the limitation of not being able to define intermolecular interactions (such as hydrogen bonding) to the index, which is important for finding QSPRs in ILs. They used their MCI as an input descriptor for a neural network that predicts viscosity with promising results for a small range of studied ILs.<sup>60</sup> However, apart from their works, MCI has not been used as input for any of the other ML studies for ILs.

Molecular descriptors, such as those discussed above, present the limitation of requiring researchers to find sets of relevant descriptors for each case and also usually they have to deal with high dimensional data. In order to overcome those problems another category of methods has been created, which works directly on molecular structures. Graph-convolution NNs transform the molecular structures to a set of neural fingerprints, which are used in order to translate structures to graphs (vectors).<sup>61</sup> A popular representation of structures uses graph nodes to represent atoms, while the edges describe bonds.<sup>62</sup> Graph theoretical approaches have been used to describe and analyse various different chemical systems.<sup>63–65</sup> The used network can be set in order to optimise the efficiency of extracted characteristics, thus improving the accuracy of the model. There are few published works on graph-based frameworks for encoding chemical structures for ILs, however these works tend to focus solely on one family of anions or cations and therefore their extension and generalisation might still be limited.<sup>66–68</sup>

Another family of descriptors used in QSPR methods are those of quantum chemical (QC) or thermodynamic nature. QC descriptors use values from quantum calculations, such as HOMO and LUMO energies, polarity, electron affinity, electronegativity *etc.*<sup>69–71</sup> Similar to the other techniques, a variety of such descriptors are calculated for a dataset of ILs with known properties and then correlation methods are used to choose those which appear to have more significant relations to the properties.<sup>72</sup> Based on QC descriptors theory, some studies have used descriptors based on COSMO-RS  $\sigma$ -profiles (molecular surface charge distributions).<sup>73</sup> COSMO-RS offers the capability of property estimation, which however requires DFT calculations that usually run on high performance computing systems.<sup>74,75</sup> Unlike DFT calculations, a pre-trained ML algorithm might be able to run on an average office computer. Stocker *et al.* recently published a very interesting study about the use of ML in chemical reaction networks, which shows that the prediction of new data points using ML methods is performed much faster than with DFT calculations, with equal accuracy.<sup>76</sup> Using COSMO-RS  $\sigma$ -profiles as data for ML methods, seems promising and has been implemented in various classical property regression models with very promising results,<sup>77–79</sup> but so far with only few implementations to ML algorithms.<sup>80–85</sup>

## Prediction of physical and chemical properties of ILs

As discussed above, ML methods are superior *versus* classical data analysis techniques in two main aspects, data



Property	IL family	Method	Distinct ILs	Training/test set points	Ref.
Viscosity	Im, Py, Quin, Pyr, Ox, Pip, Mo, Azp, Guan, N, P, S, dicationic	FFANN	1484	11031/613	53
	Im, Py, Pyr, N, P	FFANN	81	654/81	96
	Im, AA, N, Guan, Quin, Mo, Ox, P, Pip, Py, Pyr, Pyrr, S	LSSVM	443	1254/418	40
	Im, Py, Pyr, P, Quin, N	FFANN	66	612/124	99
	Im, Py, Pyr, P, N, Mo, Pip, S	ELM (FFANN)	89	1205/297	100
	Im, Py, Pyr, P, N	MLP (FFANN)	33	651/72	163
	Im, N, Py, Pyr, P, Pip, Mo, S, Cprop, Azp, Guan, Trz, Bic, Pz, Thur, Quin, thz, amd, ox, pipz, tetraz	FFANN and LSSVM	1974	1437/159 and 4479/453	97
	Im, Py, N	FFANN	31	327/31	60
Density	Im	MLP (FFANN) and RBF	n/a	317/68	93
	Im, N, Py, Pyr, P, Pip, Mo, S, Cprop, Azp, Guan, Trz, Bic, Pz, Thur, Quin, thz, amd, ox, pipz, tetraz	MLR, FFANN and LSSVM	1999	5632/625	94
	Im, Py, Pyr	FFANN	50	399/83	54
Melting point	Trz, Pyr, Py, Pip, P, Mo, Im, N, S	PLSR, SVM, RF, GBM and k-nn	2212	1486/726	88
	Im, Py, Pip, P, N	FFANN	62	50/12	87
	Im	Regression trees and SVR	281 and 134	225/22 and 107/13	90
	Trz, Pyr, Py, Pip, P, Mo, Im, N, S	KKR	2212	1770/442	92
	Im, N, P, Py, Pyr, S	PLSR, GBM, Cubist, RF, CART	467	1646/1501	164
	Py	FFANN, DT	126	n/a	47
	Guan	CPG NN	101	81/20	86
	Py	RNN	126	84/42	67
Surface tension	Im, Py, P	FFANN	79	616/132	165
Toxicity	Im, Py, Pyr, P, N, Pip, Mo, Quin, S	GFA and LSSVM	270	203/67	116
	Im, Py, Pyr, Pip, N, Quin	ELM (FFANN)	119	100/19	118
	Im, Py, Pyr, Pip, P, N, Quin	MLR and ELM	160	128/32	120
	Im, Py, Pyr, Pip, N, P, Mo	CCN and SVM	292	204/88	115
CO <sub>2</sub> solubility	Im, Py, Pyr, Pip, P, N, Mo	ELM	142	113/29	121
	Im, N, P	MLFNN (FFANN)		144 (pre-trained on H <sub>2</sub> S)	102
	Im, P, Pyr	MLP and ANFIS	14	546/182	101
	Im, N, Py, Pyr	MLR and LSSVM	21	16/5	103
	Im, N, Guan, Py, Pyr, P, Ur	PLSR, CTREE and RF	158	5424/5424	71
	Im, P	LSSVM	11	128/385	104
	Im, P	MLP	20	907/208	105
	Im, Pyr, P	DNN, RNN and CNN	13	n/a (ratio 7/3)	106
H <sub>2</sub> S solubility	Im, Pyr, P	MLP	13	595/149	166
	Im, PY, Pyr, P, N	LSSVM, MLR, RF and DT	36	1241/414	108
	Im, Py, Pyr, Pip, N, P, S	FFANN and SVM	124	8093/2023	107
	Im, N, P	MLFNN (FFANN)		513/165	102
	Im	MLFNN (FFANN)	11	372/93	109
	Im, N	ELM (FFANN)	37, 27	1025/257	84,110
	Im	ANFIS, MLP, RBF	13	554/1140	111
	Im	LSSVM	9	590/62	112
	Im	SGB (DT)	11	369/96	113
	Im, N	ELM (FFANN)	28	1055/263	114

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Venkatraman *et. al.*<sup>88</sup> (2018) investigated both linear and nonlinear approaches for the prediction of the melting points of different families of ILs, using DTs and SVM models. They used a bespoke training set of more than 2000 ILs extracted from selected papers, which they transformed to computer input using quantum mechanical descriptors obtained by computationally low-cost PM6 calculations. They compared their results to the prediction model provided by COSMO-RS. This study showed moderate absolute accuracy, but behaved well when predicting relative differences or trends in melting point differences. Following up on their study, in 2019 the same group published an extensive library of property prediction (including, but not limited to, melting point, viscosity, glass transition temperatures, density *etc.*).<sup>89</sup> The prediction was based on variety of different ML methods, from which the best performing model on each property was selected. This work is very important for property prediction, as they have created a pool of over 8 million ILs predicted properties, which can be used for guided synthesis of task-specific ILs (always taking into account possible accuracy limitations).‡

**Viscosity.** Valderrama *et al.*<sup>60</sup> (2011) were one of the first groups to investigate the prediction of viscosity trends in ILs. They trained an ANN using their MCI as input (see subsection ILs as input data) and testing the result in 26 ILs – mostly based on the imidazolium cation family. The results were satisfactory, leading to general deviations less than 5% of the experimental

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Mesbah *et. al.*<sup>105</sup> (2018) focused on the prediction of the solubility of CO<sub>2</sub> and supercritical CO<sub>2</sub> in 20 common ILs using an MLP-ANN. The authors studied a wide temperature and pressure range, 278–450 K and 0.25–100 MPa respectively. No molecular structure descriptors we used in this model either, the solubility of CO<sub>2</sub> was expressed as function of molecular weight, critical temperature and pressure of the ILs. The model

§ For CO<sub>2</sub> and H<sub>2</sub>S solubility studies, many researchers use experimentally inaccessible critical properties, boiling points or acentric factors of ILs. These properties are in fact calculated from modified Lydersen-Joback-Reid group contribution methods.<sup>285,286</sup>

**Table 2** Explanation of cations abbreviations presented in Table 1. Structures given in the ESI (see ESI)

## Toxicity

Basant *et al.*<sup>115</sup> (2015) investigated the acetyl cholinesterase enzyme (AChE) inhibition potential of ILs using SVMs. The input data were coded using Moses Descriptor Community Edition, by choosing 211 molecular descriptors. Out of those descriptors, the ones that had low variance were disregarded. The SVM outputs were compared to previously developed QSPR models and showed higher statistical confidence. Their work helped to identify which structural characteristics of the ILs are mostly responsible for AChE inhibition and also, their algorithm can be trained and generalised for more IL families easily.

Ma *et al.* published two works in 2015<sup>116,117</sup> predicting the cytotoxicity of ILs to Leukemia Rat Cell Line (IPC-81) and the ecotoxicity of ILs on *Vibrio fischeri*. The anion and cation molecular descriptors used in their studies were produced by Dragon software and included 0D–3D structural features. In both cases, the results obtained by a LSSVM nonlinear model appeared superior to the linear model, which verifies once more that the structure–property relationship is complex in the IL chemical space and simpler linear models sometimes fail to accurately predict the studied property.

Cao *et al.*<sup>118</sup> (2018) used the same dataset to predict the cytotoxicity towards Leukemia Rat Cell Line (IPC-81) using quantum chemical descriptors. They compared multiple linear regression, ELM and SVM algorithms trained on the same dataset. Their study showed that ELM has superior fitting and prediction capacity compared to their SVM (linear regression performed significantly worse than the other two) and also highlighted that the lipophilicity of the cation plays a major role in the cytotoxicity of the IL, although this was known already previously from conventional studies.<sup>119</sup> Although their results were not significantly improved compared to Ma *et al.*, this study does show that quantum chemical  $\sigma$ -profiles, can be used to model the cytotoxicity behaviour of ILs. Zhu *et al.*<sup>120</sup> (2019) expanded this work to AChE inhibition and showed that their ELM methodology can provide accurate results for ecotoxicity of ILs too. In 2020 Kang *et al.*<sup>121</sup> further progressed their work on *Vibrio fischeri* by using electrostatic potential surface area descriptors as input, thus improving the accuracy of their previously published algorithm.

## Common issues with datasets

ML correlation methods are highly dependent on the quality of the datasets, this is probably the most significant part of the algorithm, the part that makes training possible.<sup>122</sup> AI is doomed to fail if the training data are not ‘good enough’. Hence, we discuss below the parameters that make a dataset ‘good’ and how these apply to IL research. As we shall see, the composition of the ILs’ literature, which has come about through historical circumstances and was never designed for the purpose of supporting ML approaches, imposes limitations on the generalizability of results.

### Size

Unfortunately, nobody can answer the question “how much data is enough to train a ML algorithm?”, as it significantly

depends on various factors, such as the complexity of the model (*e.g.* number of inputs/outputs, the relationship between parameters, the quality of the data). Every algorithm is different and shows different sensitivity to the size of training set. A general practice followed by researchers is to try to get comparable prediction accuracy between the training and the test set. ML algorithms tend to overfit when they lack enough data, but this is not only related to the absolute number of the training data, but also to the diversity of the set, which will be further discussed below.

There are studies on the effect of training set size on QSPR models that show there is no simple correlation between the size of the set and the predictive ability of the model, but it is rather dependent on the studied property.<sup>123</sup> Obviously, if the training set includes a large percentage (*e.g.* 70%) of the total dataset, then the models usually show high predictive capabilities, but the effect of training set size reduction is not straightforward. Also, as noted by Hughes *et al.*, some properties such as melting points are more difficult to predict than others, in this case because the input descriptors can't properly describe the change in chemical interactions between solid and liquid phase.<sup>124</sup> For example, it is quite common for ILs that increasing the alkyl chain length has complex effects on the melting point, with even the direction of effect being different for shorter or longer chains, due to different preferable interactions or molecular arrangements caused by the alkyl chain itself.<sup>125,126</sup> In order for an algorithm to understand and model such complex behaviors, an adequate number or such examples in the training set is needed.

Although the appropriate size of the training dataset is very much model- and problem-specific, there are some general rules that are good for every scientist to know. Generally, a ‘too small’ training set will result in poor data prediction. A model with too many correlation parameters will overfit a small training set. On the other hand, a model with far fewer correlation parameters than needed to describe the property, is likely to underfit the training set. In both cases, the result will be predictions with high degrees of uncertainty, whose performance will significantly depend on the similarity of the test to the training set.<sup>127</sup>

### Diversity

The case of imbalanced datasets is a very common problem in data science.<sup>128</sup> In IL research imbalanced datasets can occur when the experimental data for one family of ILs (which is usually the alkylimidazolium ILs) significantly outnumber the other families. Most standard ML algorithms assume as default a properly balanced dataset and therefore it is possible that the model fits better the majority samples, while the minority cases are prone to major classification or prediction errors.<sup>129</sup>

The concept of balanced datasets is the direct response to ‘the bigger the dataset the better the algorithm will perform’. It is very important to keep a balance between creating a large and a diverse training set. Until recently, the IL community has mostly focused on alkylimidazolium salts, while other IL families came to the forefront only later. As a result, it is very



common that available physical data on alkylimidazolium ILs dominate over the others. However, creating a dataset that has over 60% data on these ILs alone, leads naturally to the algorithm overfitting on these data, giving more accurate results on imidazolium salts, but producing higher uncertainty for the other ILs. Relevant examples of this under-representation can be found in the works of Baghban *et al.*<sup>101</sup> (65% of the dataset on imidazolium ILs and the rest on different families) and Song *et al.*<sup>107</sup> (only 1 sulfonium IL from the 124 ILs of the dataset). Hence, it is always important for the reader take note of the authors description of the dataset, so that they are aware of the limitations imposed by its composition and to not over-interpret the results.

Under-representation can also exist even within an IL family. The distribution of atoms in the ILs significantly affects the chemical interactions of their ions, resulting in isomers with different physical properties. Characteristic examples are the 1-ethyl-2,3-dimethylimidazolium and 1-propyl-3-methylimidazolium bistrifluoromethylimide ILs ( $[\text{C}_2\text{C}_1\text{C}_1\text{im}][\text{NTf}_2]$  and  $[\text{C}_3\text{C}_1\text{im}][\text{NTf}_2]$ , respectively), which although they are structural isomers, have very different melting points, with  $[\text{C}_2\text{C}_1\text{C}_1\text{im}][\text{NTf}_2]$  being solid at room temperature and  $[\text{C}_3\text{C}_1\text{im}][\text{NTf}_2]$  having a melting point below  $-40^\circ\text{C}$ . In order for the algorithm to be able to correlate the properties to the given structures and make accurate predictions in such cases, all types of isomers should be equally (or at least comparably) represented in the datasets.

In order to make our case about under-representation of ILs clearer, we estimated the whole chemical space of isomers that encloses a specific dataset. We implemented Pólya's method to enumerate the number of isomers for acyclic alkyl chains as a function of the number of carbon atoms, which was taken from Fujita's work.<sup>130</sup> This method does not take into account stereoisomerism (enantiomers and diastereomers), and therefore, the number obtained thereof represents only the lower limit of the total numbers of possible isomers. However, highly strained branched alkyl substituents which might not be thermodynamically stable, such as those analogous to *tert*-butyl,

were not excluded from the count, but they represent only a marginal fraction of the total.<sup>131</sup> Details about the enumeration method are further discussed in the ESI.†

As a basis for this analysis we used the work of Paduszyński,<sup>97</sup> as it is one of the largest and most diverse datasets of all the published works. Fig. 7 and 8 show the cases of two of the most widely studied families of ILs, imidazolium and ammonium-based cations. The profile is very similar for all the presented cases, for smaller numbers of side-chain carbons ( $<4$  carbons) the training set occupies a satisfactory percentage of the chemical space (in some cases up to 70%), while for larger numbers of carbons ( $>10$  carbons) typically there are only a couple of studied IL. This behaviour is expected, as longer-chain ILs are usually more difficult to synthesise, so the available physical data on those are very limited.

To understand the impact of this, the algorithm will try to predict a chemical space of  $10^8$  ILs, based only on 1 or 2 representative examples. As a result, the model will probably try to extrapolate the behaviour of these isomers from the behaviour of the better-represented small carbon number space. Here we face a very interesting question, will a change in the distribution of carbons on an alkyl chain affect the properties the same way for an IL with 10 carbons as for an IL with 4? Will changing the distribution of carbons on an alkyl chain affect the properties of a low- and a high-molecular weight IL in an analogous way? To our knowledge there is no available published work responding to these questions, therefore it is unknown whether making the assumption that they will can be safely used for the extrapolation of the behaviour of ILs. As will be discussed further below, extrapolation is not a wise choice in ML models, especially when based on such uncertainties. It is also important to point out that in our calculations we only explored the chemical space created by the structural isomers of the cations. Since the properties of ILs come as a result of cation-anion combinations, by introducing different anions the chemical spaces are automatically increased by many orders of magnitude. The number of structural isomers (excluding enantiomers and diastereomers) for the imidazolium cation

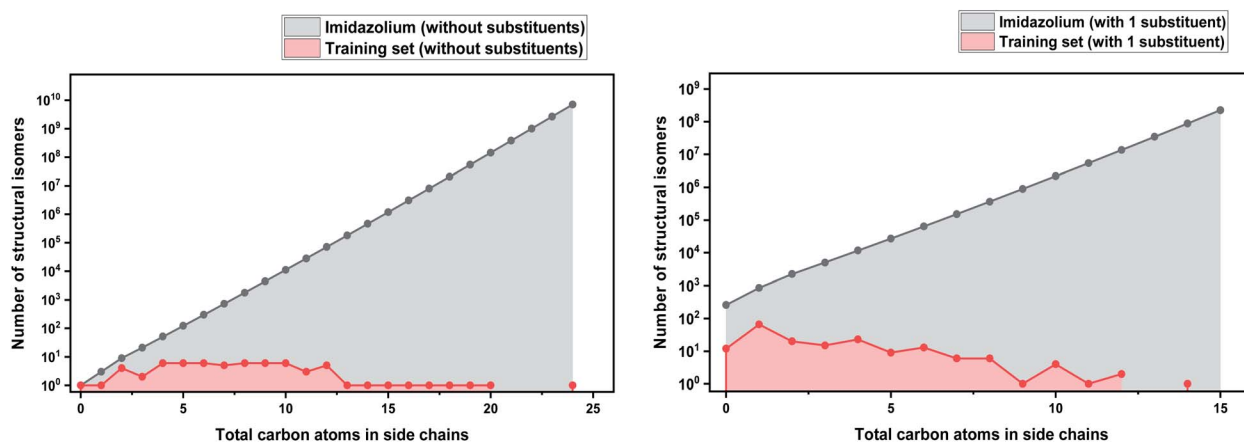
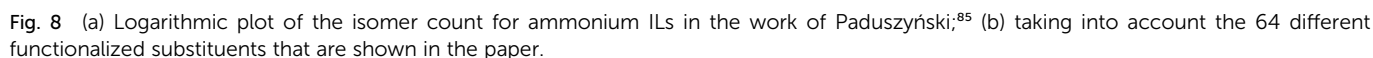


Fig. 7 (a) Logarithmic plot of the isomer count for imidazolium cations in the work of Paduszyński;<sup>95</sup> (b) taking into account the 86 different functionalized substituents that are shown in the paper.





In order for results to be reproducible, the ILs have to be either ultrapure (<0.1% of impurity levels)<sup>139</sup> or the level of purity has to be clearly stated in each work. This has become more common in works published in the last few years, but

Another factor which falls under the data quality category, is how representative is the training set of the studied chemical space. It is fundamental in data science to use the ML results only for interpolation of experimental values. Extrapolation is not a good practice, since many common ML methodologies function as ‘black-boxes’, the researcher can never be certain of the true equation hidden behind a NN. A very characteristic example of the poor extrapolation potential of ML is presented by Pavlo Dral for the simple function of  $|x|^{0.5}$  (Fig. 9).<sup>141</sup>

The difficulty in extracting consistent, high quality data from the literature leads to the possibility of collecting bespoke data sets as inputs for ML approaches. Recent years have seen incredible advances in high throughput experimental techniques.<sup>145–147</sup> Attempts have been made to apply high throughput techniques to the measurement of physical data for ILs<sup>148–150</sup> and to couple this with ML.<sup>151</sup> However, the range of ionic liquids to which this has been applied has been restricted by the multistep synthesis and complex purification that many ILs require. Hence, these attempts have been restricted to those ILs that are synthetically more accessible, such as protic ILs.<sup>152,153</sup> As has been described above, one cannot simply extrapolate these results to other families of ILs. Another very useful alternative is the design and use of automated robotic platforms, which could synthesise and/or test the physical properties of the studied systems.<sup>154</sup> These platforms, although they are capable of collecting huge amounts of data in short times, in the case of ILs would still be delayed by synthesis and purification procedures.

Figure 1 shows a plot of the true function, training data, and the ML function. The x-axis ranges from -10 to 10, and the y-axis ranges from -5 to 3. The true function is a black curve, the training data is red dots, and the ML function is a blue curve. The ML function is a smooth approximation of the true function, trained on the data points.

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synthetic procedures,<sup>161,162</sup> however to our knowledge this hasn't yet been expanded to the IL area.

## Machine learning for molecular dynamics simulations

Machine learning still has to gain traction in the ionic liquid community. In this section, we will compare machine learning to a well-established theoretical method, that of molecular dynamics (MD) simulation. Molecular dynamics uses numerical integration of Newton's equations of motion to predict how the positions of atoms (or groups of atoms) evolve over time. Statistical thermodynamics is then used to derive macroscopic properties, both structural and dynamic. An MD simulation thus typically consists of the steps shown in Fig. 10, and ML can be used to enhance virtually every aspect of MD. Naturally, 'Machine Learning' is a much more general term, and encompasses methods that can be seen as a sophisticated tool for fitting and statistical analysis. We will give a brief overview here of the use of molecular dynamics in ionic liquids, how it differs from machine learning methods, and how the two approaches can be used synergistically. The ML examples we present are largely from outside the field of ionic liquids, but the general concepts can and undoubtedly will be used for ionic liquids as well. A good overview of the approaches presented in this section can be found in ref. 141,<sup>167–169</sup>.

Over the past two decades, MD simulations have substantially advanced the understanding of ionic liquids by modelling the structure and dynamics of the liquid phase.<sup>170–172</sup> Many ionic liquids, in particular those with long alkyl or perfluoroalkyl side chains, show pronounced nanosegregation into polar, non-polar, and in some cases fluorinated domains.<sup>172</sup> MD simulations provided invaluable insight into how and when these domains form.<sup>173–180</sup> Even in cases where the liquid structure can be probed experimentally with scattering experiments, MD simulations are required to trace back the observed features to structural motifs on the molecular scale.<sup>181,182</sup> One of the crucial

advantages here is that MD simulations based on classical force fields allow for targeted modifications which are not possible experimentally. For example, several groups used MD simulations with artificial, deliberate changes in the dihedral parameters to increase the barriers for rotation around specific bonds, thus separating out the effects of conformational flexibility.<sup>183–186</sup>

Despite the astounding successes of classical MD simulations, one of the central problems remains the choice of a force field, *i.e.* the first step in Fig. 10. MD simulations rely on the availability of accurate forces and energies as a function of atomic positions. For ionic liquids in particular, polarizability is more and more recognised as an essential element for the accurate prediction of structure and dynamics.<sup>178,187–192</sup> It is to some degree possible to mimic the effects of electronic polarizability with scaled charges, however this comes at the expense of lost accuracy.<sup>193,194</sup> Even in cases where explicit treatment of polarizability is not necessary, choosing a reasonable set of atomic charges along with well-balanced bonded parameters is a nontrivial task.<sup>195–199</sup> The vast number of possible ionic liquids is yet another serious challenge for force field development, and transferable force fields are required to not be limited to one particular system.<sup>195,200–207</sup>

Molecular dynamics simulations can be used to predict a wide range of properties of ionic liquids from thermal transitions to transport, structural, or spectroscopic properties.<sup>74,199,208–216</sup> The prediction of properties with MD simulations has two facets. First, the predicted property can be compared with known experimental values to validate the method or force field, similar to the test sets for ML algorithms.<sup>217,218</sup> Properties such as density, self-diffusion coefficients or surface tension are commonly used for this purpose.<sup>210,211,215,219,220</sup> Good agreement between experiment and MD simulation suggests that the relevant physics are reasonably reflected by the model, which is then used to either gain mechanistic understanding or to predict a different property. The second facet is thus the use of MD simulations to predict hitherto unknown properties. Similar problems to ML methods arise in the sense that the

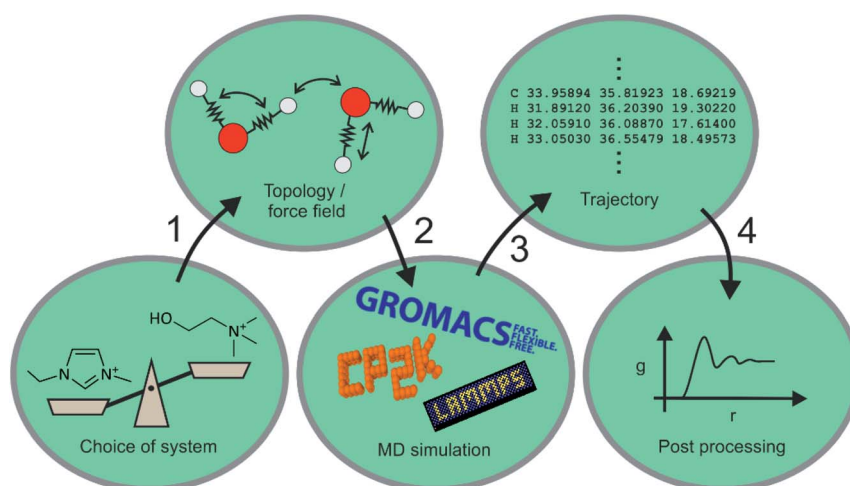


Fig. 10 Typical steps of an MD simulation.

more widely applicable models (*i.e.* generic classical force fields) perform poorly for quantitative predictions, whereas interpolation of properties of similar compounds can be done much more reliably. An exception are *ab initio* MD simulations, which do not rely on a force field and can be used to predict ionic liquid properties, if sufficient computational resources are available.<sup>74,208,209,221</sup>

One way in which MD simulations and machine learning can be used synergistically is to automate the construction of force fields, an otherwise complex and laborious task. Broadly speaking, machine learning as an advanced ‘fitting tool’ can be used to obtain a force field by fitting forces and/or energies.<sup>167,222–225</sup> Thus, machine learning interatomic potentials (MLIP) are usually trained on high-level *ab initio* methods to yield accurate energies (and forces) as a function of atomic coordinates.<sup>226–230</sup> An example are High Dimensional Neural Network Potentials (HDNNP), which aim to fully replace the *ab initio* method once trained.<sup>222,231–233</sup> The MLIP can be re-trained ‘on the fly’ every few steps using a high level *ab initio* method.<sup>233–235</sup> This implementation avoids the issues associated with extrapolation (as described in the previous section), a good illustrative example is given by Botu and Ramprasad,<sup>235</sup> as well as in Fig. 11. However for all MLIP, some effort has to be made to incorporate physical constraints such as conserved quantities or invariance with respect to rotation and exchange of identical particles.<sup>167,223,236</sup>

Purely *ab initio* molecular dynamics – as opposed to those based on classical force fields – become more and more feasible for ionic liquids, but remain computationally expensive.<sup>205,208,237</sup> Machine learning can be of use to enhance and accelerate the quantum chemical method itself, rather than providing a complete substitute such as in MLIP.<sup>168,238</sup> For example, a  $\Delta$ -learning scheme can be used which learns only the difference between a cheap low level method (semi-empirical, classical,

*etc.*) and an accurate high level method (DFT, post-HF *etc.*).<sup>168,239–242</sup>

Just as important as the simulation itself is the final step shown in Fig. 10, *i.e.* the post processing of the trajectory. Analysis tools such as TRAVIS<sup>243,244</sup> are invaluable to extract structural and dynamic information from a trajectory which by itself does not provide information to a human reader. Purposeful post processing and visualisation is crucial to understand the behaviour of bulk ionic liquids by means of MD simulation.<sup>245–247</sup> MD simulations can thus serve as a bridge between molecular features and bulk properties.<sup>248,249</sup>

The high dimensionality of an atomistic trajectory can in some cases be reduced to just a few dimensions which can be understood by a human. Such low dimensional collective variables have already been used to describe nucleation and solute conformations in ionic liquids.<sup>250–252</sup> ML can be employed to find collective variables to describe complex transitions, which can then be used to bias and analyse the system.<sup>169</sup>

Furthermore, there are several studies where machine learning has been used to extract information from or in combination with an MD simulation. In a recent publication, Jung and Yethiraj used a deep neural network DNN to predict the phase diagrams of mixtures of ionic liquids with poly(ethylene oxide).<sup>253</sup> An example outside the ionic liquid community is the decomposition of 1,2-dioxetane, which has been investigated using *ab initio* MD simulation.<sup>254,255</sup> Machine learning models were then used to identify the required conditions for different decomposition pathways and lifetimes.<sup>254,255</sup> This example shows that machine learning can indeed provide conceptual insights.

To conclude this section, we would like to consider the bigger picture, *i.e.* the purpose of the process shown in Fig. 10. Many MD simulations in the ionic liquid community are used to understand a well characterised system, rather than as an actual prediction tool for the unknown. Machine learning, on the other hand, is often used as an interpolation or ‘fitting’ tool trained on an experimental database. However, ML and MD can also be combined to take advantage of each. For example, MD simulations are well suited to study electrostatic screening in ionic liquids.<sup>256,257</sup> Although not specific to ionic liquids, Kadupitiya *et al.* developed a ML model to predict the ion density profile of a confined electrolyte.<sup>258–260</sup> The ML model was trained on MD simulations and takes simple parameters as input, such as the concentration of a salt, the confinement length, or the ion diameters.<sup>258</sup>

Machine learning can be used to enhance molecular dynamics simulations and *vice versa*. The examples outlined above show the great benefits of such a synergistic combination, exploiting the strengths of each method and avoiding their weaknesses. It is without doubt that the exciting advances made by machine learning will be used increasingly by the ionic liquid community, once knowledge spreads and the required algorithms become implemented in common software packages. Machine learning promises faster and more accurate simulations as well as new tools for the interpretation of results, and the future will show to what degree these promises translate to practise.

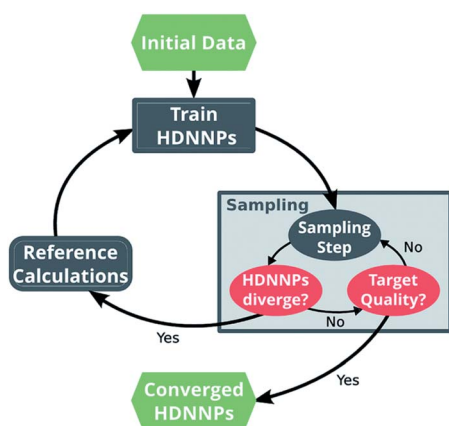


Fig. 11 Scheme of the general approach to automatically construct a force field using ML, in this case HDNNP. The ML algorithm is trained using the output (forces, energies) of a more expensive higher level method. The simulation is evolved using the MLIP, and re-trained every few steps to avoid extrapolation. Once converged, the computationally inexpensive MLIP can be used for production purposes. Reprinted by Gastegger *et al.*<sup>233</sup> – published by The Royal Society of Chemistry.



## Future aspects

Research to date on the applications of ML algorithms to ionic liquids has proven that these are competitive with other computational algorithms in terms of classification and can provide excellent prediction capacity (within the constraints described above). Indeed, the majority of studies (see Table 1) had this as their primary objective, or in some cases to compare the effectiveness of different ML approaches to provide such predictions. However, there is much more they can offer. ML models generally show a trade-off between transparency of their decision-making process and the accuracy of prediction. For example, DTs offer incredible possibilities for the user in terms of understanding and post-processing the decision making process, however they are not able to generate such complex correlations as DNNs – which in their majority still have to be considered as ‘black boxes’ and be trusted without investigating how they reached a result.<sup>261,262</sup>

Understanding the intermediate steps of the decision-making process could prove extremely beneficial for the IL research field. Working in the basis of physical sciences research, researchers are trying to interpret the natural phenomena and model them mathematically in order to predict the behaviour of the studied, as well as unknown systems. ML can help with that, because it offers the advantage that it doesn't need to understand chemistry in order to detect correlations. Given a dataset of independent measurements, we can train an algorithm that will eventually manage to identify the relevant features that significantly contribute to the studied property.

Explainable AI (XAI) refers to the process of creating AI models which use interpretable parameters as part of their decision-making process.<sup>263</sup> The significance of this is enormous, starting with data protection and copyrights. As per 2018, according to General Data Protection Regulation (GDPR)

citizens of EU are granted the “right to explanation” if they are affected by a decision-making algorithm.<sup>264</sup> Obviously, this right cannot be claimed when the complexity of an AI algorithm obscures the rationale behind the recommended decision.

XAI practises can have a significant impact on chemical research, as they can help researchers to improve their understanding and knowledge on the investigated properties or processes.<sup>265</sup> In IL research there have been some initial attempts to explain the effect of specific parameters for simpler (first order) linear regression algorithms.<sup>107</sup> Greaves *et al.* used two different ML algorithms, a NN and a multiple linear regression algorithm to predict the reaction rate of a bimolecular nucleophilic substitution in different ILs. In their work they showed that, although NN gives the best statistical fitting, it doesn't give the possibility of judging which descriptors are significant. On the other hand, the linear regression algorithm, which also provides adequate results, clearly shows which descriptors mostly affect the model.<sup>56</sup> According to their study, the reaction rate is mostly affected by three cation descriptors, namely the number of secondary sp<sup>3</sup> hybridised carbons, the number of rotatable bonds and molar refractivity.

While using first-order models allows easier understanding of the significant contributions to any property, due to the simplicity of their nature; the same simplicity means that this comes at the cost of lower accuracy in predicting complex behaviours, such as viscosity. Low *et al.* very accurately state in their work that many semi-empirical predictions could likely be refined by using a higher level of theory during initial parameter selection, instead of using the arbitrarily-engineered features that are popular in many models.<sup>92</sup> In practise this would mean choosing IL descriptors that are based on distinctive properties (such as HOMO–LUMO gap, or  $\sigma$ -profiles) instead of an artificial representation that has no meaning in physical space (such as SMILES descriptors).

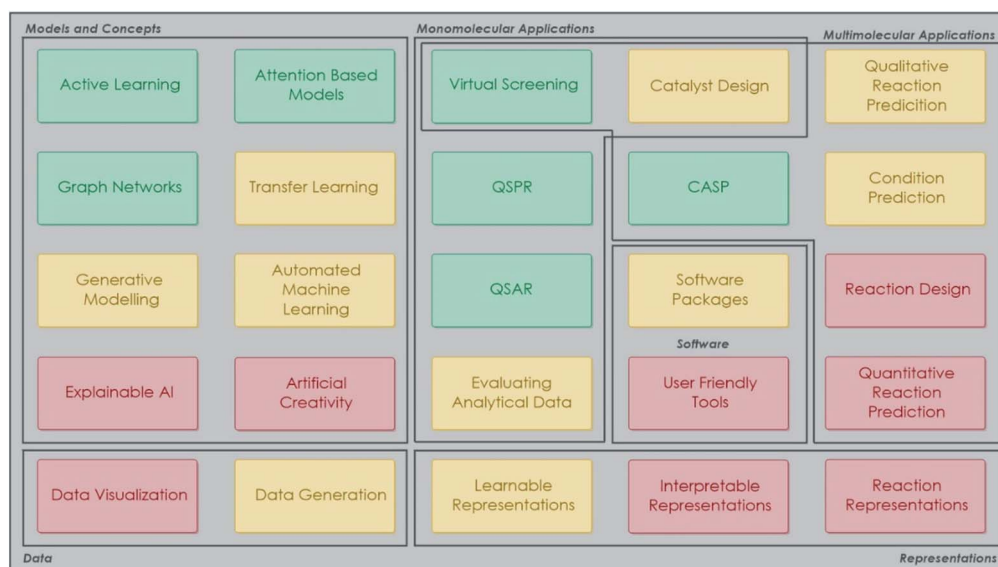


Fig. 12 Subtopics of ML applications for chemistry research, categorised by the number of published works. Red: highly underexplored; yellow: some attempts demonstrated; green: fields of major attention. Reprinted by Pflüger and Glorius<sup>267</sup> – Published by John Wiley & Sons.

It is true that there is an infinite space of unexplored possibilities to use AI not just for predicting, but also for enhancing our understanding of ‘hidden’ factors affecting physical and chemical processes, which is yet not reachable (Fig. 12). However, in the near future, these problems will be overcome. New generations of scientists will be far more familiar with those methods and will be more multidisciplinary trained and able to analyse and understand the results. The preliminary work that is currently conducted will create a solid basis in order for deeper exploration and understanding of the underlying knowledge.

Over the past few years, ML-based research has expanded to complex ionic systems and, eventually, to ILs. The majority of published works in this field explore the use of ML techniques either for the prediction of their physical properties, or for solubility of gases in ILs, with the purpose of the study being to demonstrate that ML can be a useful tool. Others have compared how different ML algorithms have performed for

Finally, we would like to conclude this work with a look into the future. All the cases described above are about the simplest

case of having neat ILs. However, there is the growing interest in using mixtures of ILs with molecular solvents or other ILs in order to overcome common problems (such as high viscosity).<sup>277</sup> However, these new solvent systems are extremely complicated and require a thorough characterisation on their own. Optimising such systems creates a complex chemical space, whose exploration dramatically increases the number of experimental measurements, as changing the composition of the mixture dramatically alters its properties. Therefore, there is an urgent need to minimise the number of samples that are needed in order to have an accurate representation of the space (DoE and high throughput screening).<sup>278</sup> There are only limited published works on ML-assisted screening of such complex mixtures,<sup>151,279–281</sup> but this is certainly one of the areas where ML models can flourish.<sup>282</sup> Similarly to the case of MD simulations, combining different methods can certainly enhance their capabilities, but requires a great amount of expertise and interdisciplinarity. Someone could say that we are still in the prehistoric period of ML-aided research, although much effort is given in order to include such models in commercial software packages. One thing is certain, once ML models become broadly available to users, they will completely change data analysis and experimental design. Automated robots that perform complex tasks, while getting feedback from ML models in order to improve their output have already been created and show extraordinary results.<sup>283</sup>

## Author contributions

Conceptualization S. K., T. W.; supervision T. W.; writing – original draft preparation S. K., F. P., F. M.; writing – review & editing S. K., F. P., F. M., T. W.

## Conflicts of interest

There are no conflicts to declare.

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